

Mouse Sox9 Sequence

```

1  AGTTTCAGTC CAGGAAC TTT TCTTTGCAAG AGAGACGAGG TGCAAGTGGC
51  CCCGGTTTCG TTCTCTGTTT TCCCTCCCTC CTCCTCCGCT CCGACTCGCC
101 TTCCCCGGGT TTAGAGCCGG CAGCTGAGAC CCGCCACCCA GCGCCTCTGC
151 TAAGTGCCCC CCGCCGCAGC CCGGTGACGC GCCAACCTCC CCGGGAGCCG
201 TTCGCTCGGC GTCCGCGTCC GGGCAGCTGA GGAAGAGGA GCCCCAGCCG
251 CCGCGGCTTC TCGCCTTTCC CGGCCACCCG CCCCCTGCCC CGGGCTCGCG
301 TATGAATCTC CTGGACCCCT TCATGAAGAT GACCGACGAG CAGGAGAAGG
351 GCCTGTCTGG CGCCCCCAGC CCCACCATGT CGGAGGACTC GGCTGGTTCC
401 CCCTGTCCCT CGGGCTCCGG CTCGGACACG GAGAACACCC GGCCCCAGGA
451 GAACACCTTC CCCAAGGGCG AGCCGGATCT GAAGAAGGAG AGCGAGGAAG
501 ATAAGTTCCC CGTGTGCATC CGCGAGGCGG TCAGCCAGGT GCTGAAGGGC
551 TACGACTGGA CGTGGTGCC CATGCCCCGTG CGCGTCAACG GCTCCAGCAA
601 GAACAAGCCA CACGTCAAGC GACCCATGAA CGCCTTCATG GTGTGGGCGC
651 AGGCTGCGCG CAGGAAGCTG GCAGACCAGT ACCCGCATCT GCACAACGCG
701 GAGCTCAGCA AGACTCTGGG CAAGCTCTGG AGGCTGCTGA ACGAGAGCGA
751 GAAGAGACCC TTCGTGGAGG AGGCGGAGCG GCTGCGCGTG CAGCACAAGA
801 AAGACCACCC CGATTACAAG TACCAGCCCC GGCGGAGGAA GTCGGTGAAG
851 AACGGACAAG CGGAGGCCGA AGAGGCCACG GAACAGACTC ACATCTCTCC
901 TAATGCTATC TTCAAGGCGC TGCAAGCCGA CTCCCCACAT TCCTCCTCCG
951 GCATGAGTGA GGTGCACTCC CCGGGCGAGC ACTCTGGGCA ATCTCAGGGT
1001 CCGCCGACCC CACCCACCAC TCCCAAAACC GACGTGCAAG CTGGCAAAGT
1051 TGATCTGAAG CGAGAGGGGC GCCCTCTGGC AGAGGGGGGC AGACAGCCCC
1101 CCATCGACTT CCGCGACGTG GACATCGGTG AACTGAGCAG CGACGTCATC
1151 TCCAACATTG AGACCTTCGA CGTCAATGAG TTTGACCAAT ACTTGCCACC
1201 CAACGGCCAC CCAGGGGTTT CGGCCACCCA CGGCCAGGTC ACCTACACTG
1251 GCAGTTACGG CATCAGCAGC ACCGCACCCA CCCCTGCGAC CGCGGGCCAC

```

Figure 1(a)

1301 GTGTGGATGT CGAAGCAGCA GGC GCCGCC CCTCTCCGC AGCAGCCTCC
 1351 GCAGGCCCCG CAAGCCCCAC AGGCGCCTCC GCAGCAGCAA GCACCCCCGC
 1401 AGCAGCCGCA GGCACCCAG CAGCAGCAGG CACACACGCT CACCACGCTG
 1451 AGCAGCGAGC CAGGCCAGTC CCAGCGAACG CACATCAAGA CGGAGCAGCT
 1501 GAGCCCCAGC CACTACAGGG AGCAGCAGCA GCACTCCCCG CAACAGATCT
 1551 CCTACAGCCC CTTCACCTT CCTCACTACA GGCCCTCCTA CCCGCCCATC
 1601 ACCCGTTTCG AATACGACTA CGCTGACCAT CAGAACTCCG GCTCCTACTA
 1651 CAGTCACGCA GCCGGCCAGG GCTCAGGGCT CTACTCCACC TTCACTTACA
 1701 TGAACCCCGC GCAGCGCCCC ATGTACACCC CCATCGGTGA CACCTCCGGG
 1751 GTCCCTTCCA TCCCGCAGAC CCACAGCCCG CAGGACTGGG AACAAACAGT
 1801 CTACACACAG GTCACCAGAC CCTGAGAAGA GAAAAGCTAT GGTGACAGAG
 1851 CTGATCTTTT TTTT TTTT TTTTAAAGA AGAAAAGAAA GAAACGAAAA
 1901 AGAAAAAGCT GAAGGAAATC AAGAACCAAT TGAAATTCCT TTGGACACTT
 1951 TTTT TTTTGT CCTTTCGTTA ATTTTAAAA GACATGTAAA GGAAGGTAAC
 2001 GATTGCTGGG CATTCCAGGA GAGAGACTTT AAGACTTTGT CTGAGCTCAT
 2051 GACAACATAT TGCAAATGGC CGGGCCACTC GTGGCCAGAC GGACAGCACT
 2101 CCTGGCCAGA TGGACCCACC AGTATCAGCG AGGAGGGGCT TGTCTCCTTC
 2151 AGAGTTAACA TGGAGGACGA TTGGAGAATC TCCCTGCCTG TTTGGACTTT
 2201 GTAATTATTT TTTAGCCGTA ATTAAAGAAA AAAAAAGTCC AAAAAAAA

Figure 1(b)

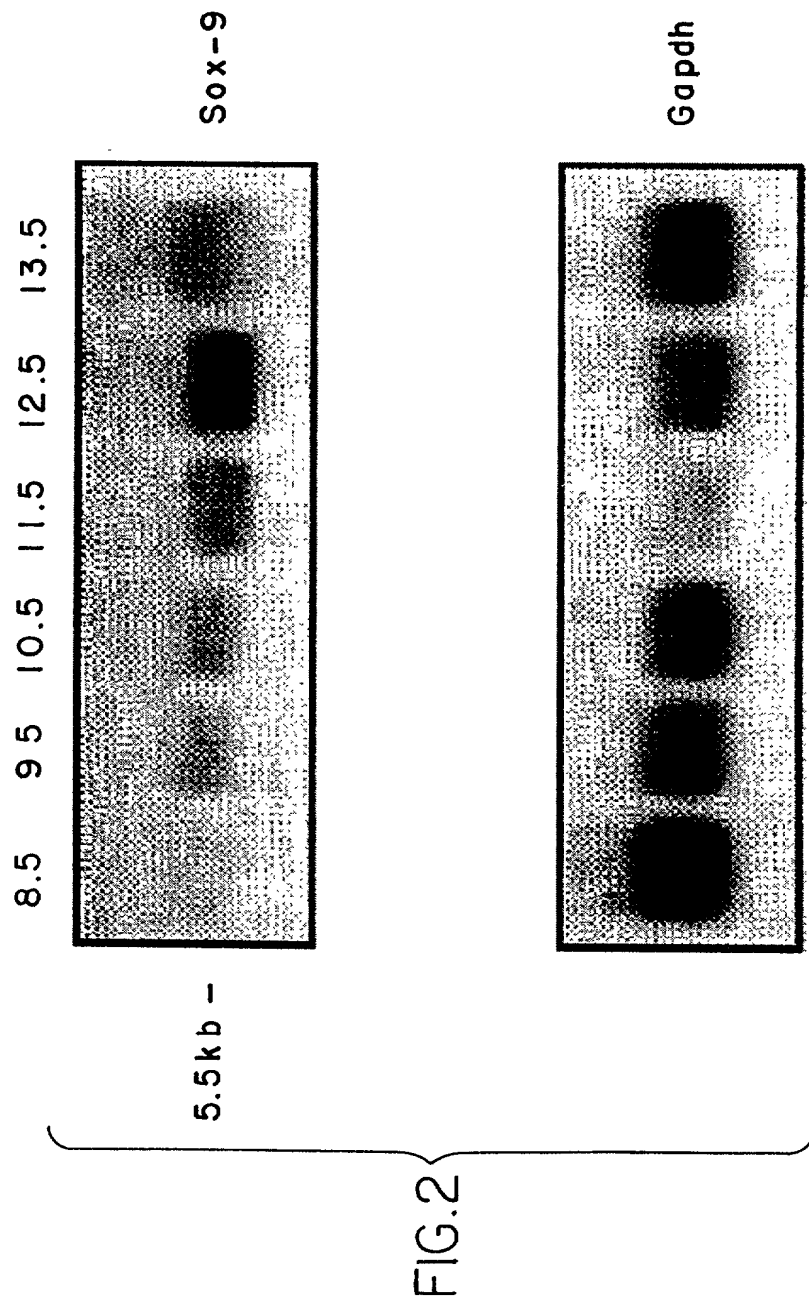
Mouse Sox-9 amino acid sequence

Met	Asn	Leu	Leu	Asp	Pro	Phe	Met	Lys	Met	Thr	Asp	Glu	Gln	Glu	Lys	1	5	10	15
Gly	Leu	Ser	Gly	Ala	Pro	Ser	Pro	Thr	Met	Ser	Glu	Asp	Ser	Ala	Gly	20	25	30	
Ser	Pro	Cys	Pro	Ser	Gly	Ser	Gly	Ser	Asp	Thr	Glu	Asn	Thr	Arg	Pro	35	40	45	
Gln	Glu	Asn	Thr	Phe	Pro	Lys	Gly	Glu	Pro	Asp	Leu	Lys	Lys	Glu	Ser	50	55	60	
Glu	Glu	Asp	Lys	Phe	Pro	Val	Cys	Ile	Arg	Glu	Ala	Val	Ser	Gln	Val	65	70	75	80
Leu	Lys	Gly	Tyr	Asp	Trp	Thr	Leu	Val	Pro	Met	Pro	Val	Arg	Val	Asn	85	90	95	
Gly	Ser	Ser	Lys	Asn	Lys	Pro	His	Val	Lys	Arg	Pro	Met	Asn	Ala	Phe	100	105	110	
Met	Val	Trp	Ala	Gln	Ala	Ala	Arg	Arg	Lys	Leu	Ala	Asp	Gln	Tyr	Pro	115	120	125	
His	Leu	His	Asn	Ala	Glu	Leu	Ser	Lys	Thr	Leu	Gly	Lys	Leu	Trp	Arg	130	135	140	
Leu	Leu	Asn	Glu	Ser	Glu	Lys	Arg	Pro	Phe	Val	Glu	Glu	Ala	Glu	Arg	145	150	155	160
Leu	Arg	Val	Gln	His	Lys	Lys	Asp	His	Pro	Asp	Tyr	Lys	Tyr	Gln	Pro	165	170	175	
Arg	Arg	Arg	Lys	Ser	Val	Lys	Asn	Gly	Gln	Ala	Glu	Ala	Glu	Glu	Ala	180	185	190	
Thr	Glu	Gln	Thr	His	Ile	Ser	Pro	Asn	Ala	Ile	Phe	Lys	Ala	Leu	Gln	195	200	205	
Ala	Asp	Ser	Pro	His	Ser	Ser	Ser	Gly	Met	Ser	Glu	Val	His	Ser	Pro	210	215	220	
Gly	Glu	His	Ser	Gly	Gln	Ser	Gln	Gly	Pro	Pro	Thr	Pro	Pro	Thr	Thr	225	230	235	240
Pro	Lys	Thr	Asp	Val	Gln	Ala	Gly	Lys	Val	Asp	Leu	Lys	Arg	Glu	Gly	245	250	255	
Arg	Pro	Leu	Ala	Glu	Gly	Gly	Arg	Gln	Pro	Pro	Ile	Asp	Phe	Arg	Asp	260	265	270	

Figure 1(c)

Val	Asp	Ile	Gly	Glu	Leu	Ser	Ser	Asp	Val	Ile	Ser	Asn	Ile	Glu	Thr	275	280	285	
Phe	Asp	Val	Asn	Glu	Phe	Asp	Gln	Tyr	Leu	Pro	Pro	Asn	Gly	His	Pro	290	295	300	
Gly	Val	Pro	Ala	Thr	His	Gly	Gln	Val	Thr	Tyr	Thr	Gly	Ser	Tyr	Gly	305	310	315	320
Ile	Ser	Ser	Thr	Ala	Pro	Thr	Pro	Ala	Thr	Ala	Gly	His	Val	Trp	Met	325	330	335	
Ser	Lys	Gln	Gln	Ala	Pro	Pro	Pro	Pro	Pro	Gln	Gln	Pro	Pro	Gln	Ala	340	345	350	
Pro	Gln	Ala	Pro	Gln	Ala	Pro	Pro	Gln	Gln	Gln	Ala	Pro	Pro	Gln	Gln	355	360	365	
Pro	Gln	Ala	Pro	Gln	Gln	Gln	Gln	Ala	His	Thr	Leu	Thr	Thr	Leu	Ser	370	375	380	
Ser	Glu	Pro	Gly	Gln	Ser	Gln	Arg	Thr	His	Ile	Lys	Thr	Glu	Gln	Leu	385	390	395	400
Ser	Pro	Ser	His	Tyr	Arg	Glu	Gln	Gln	Gln	His	Ser	Pro	Gln	Gln	Ile	405	410	415	
Ser	Tyr	Ser	Pro	Phe	Asn	Leu	Pro	His	Tyr	Arg	Pro	Ser	Tyr	Pro	Pro	420	425	430	
Ile	Thr	Arg	Ser	Glu	Tyr	Asp	Tyr	Ala	Asp	His	Gln	Asn	Ser	Gly	Ser	435	440	445	
Tyr	Tyr	Ser	His	Ala	Ala	Gly	Gln	Gly	Ser	Gly	Leu	Tyr	Ser	Thr	Phe	450	455	460	
Thr	Tyr	Met	Asn	Pro	Ala	Gln	Arg	Pro	Met	Tyr	Thr	Pro	Ile	Gly	Asp	465	470	475	480
Thr	Ser	Gly	Val	Pro	Ser	Ile	Pro	Gln	Thr	His	Ser	Pro	Gln	Asp	Trp	485	490	495	
Glu	Gln	Pro	Val	Tyr	Thr	Gln	Val	Thr	Arg	Pro						500	505		

Figure 1(d)



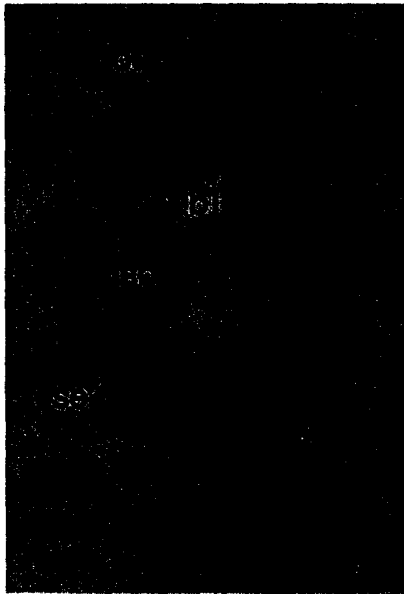


FIG. 3a

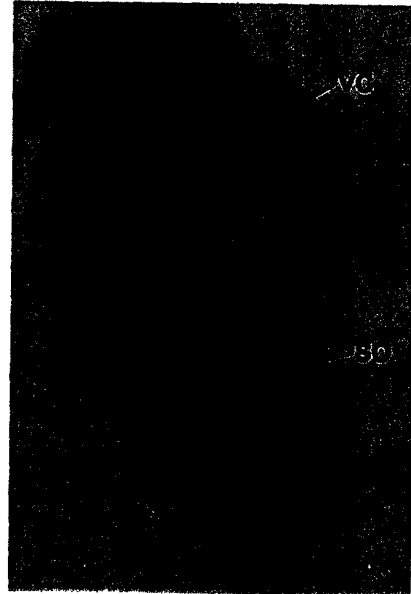


FIG. 3b

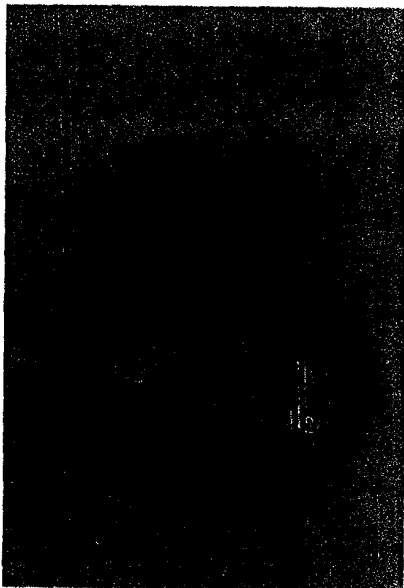


FIG. 3c

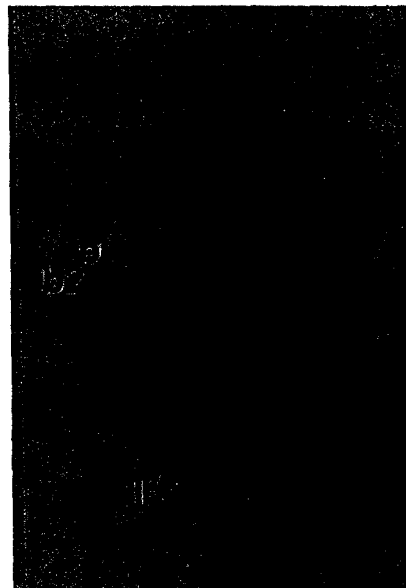


FIG. 3d

[illegible]

OC

1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 26

FIG.3h

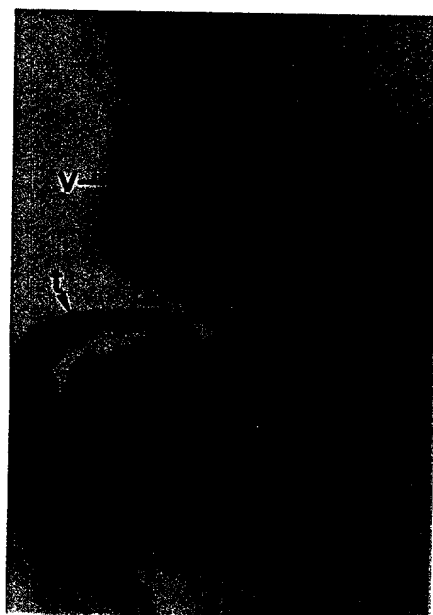


FIG.3i

00010007 072004

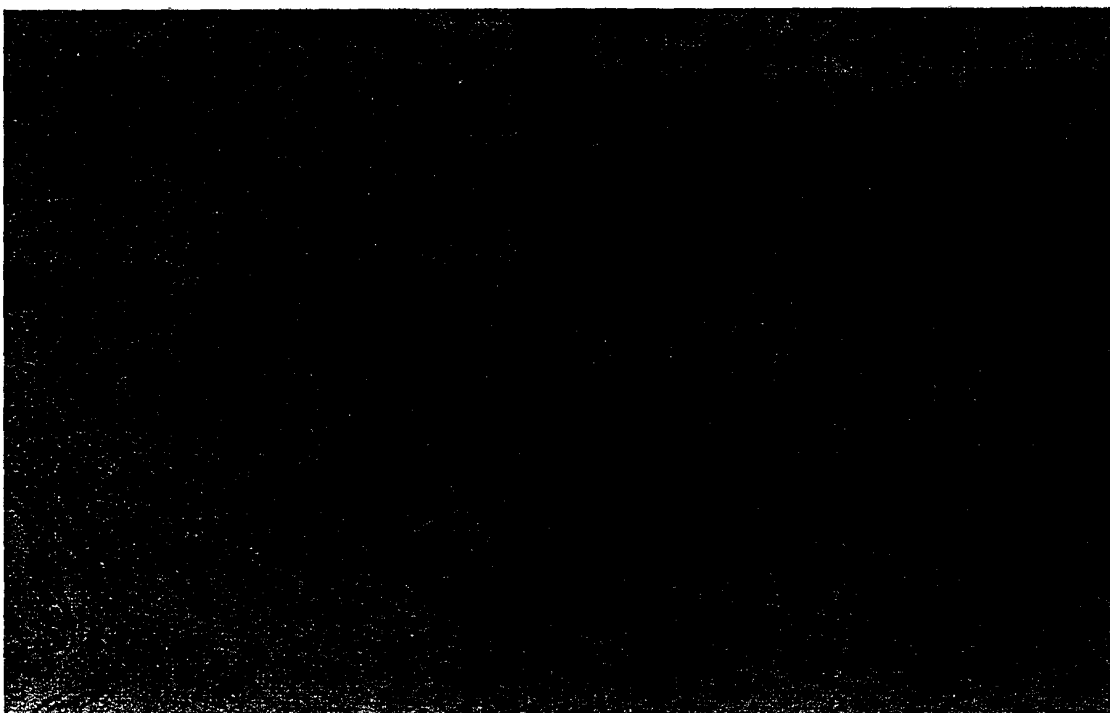


FIG.4

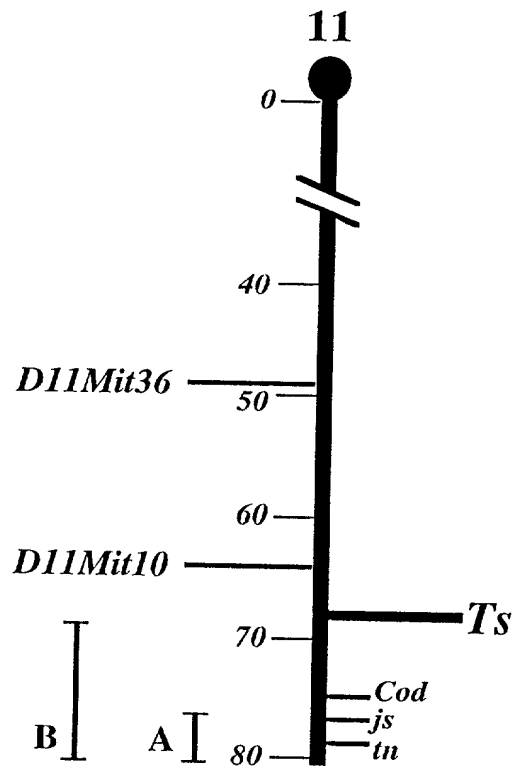


FIG.5

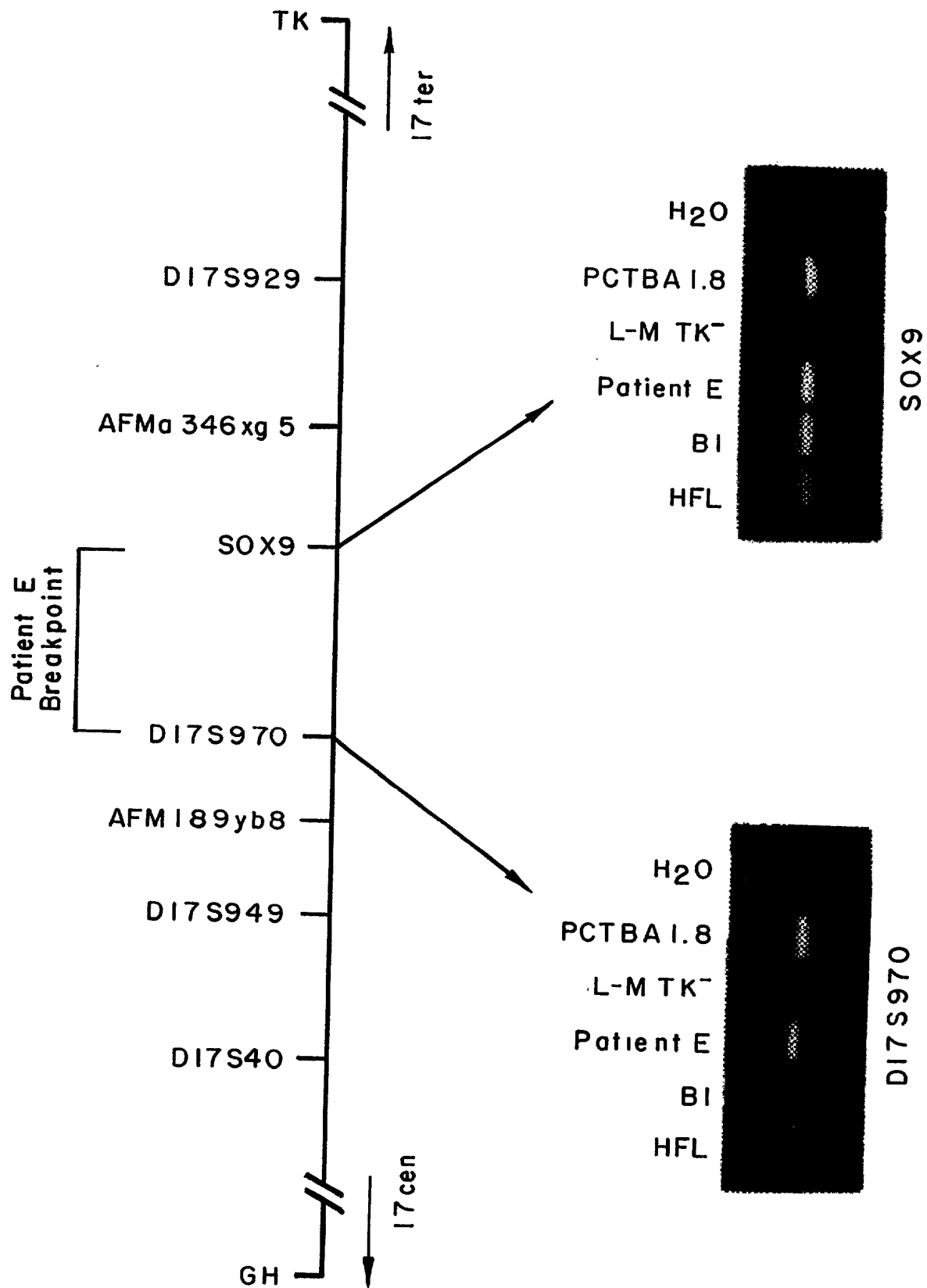


FIG. 6

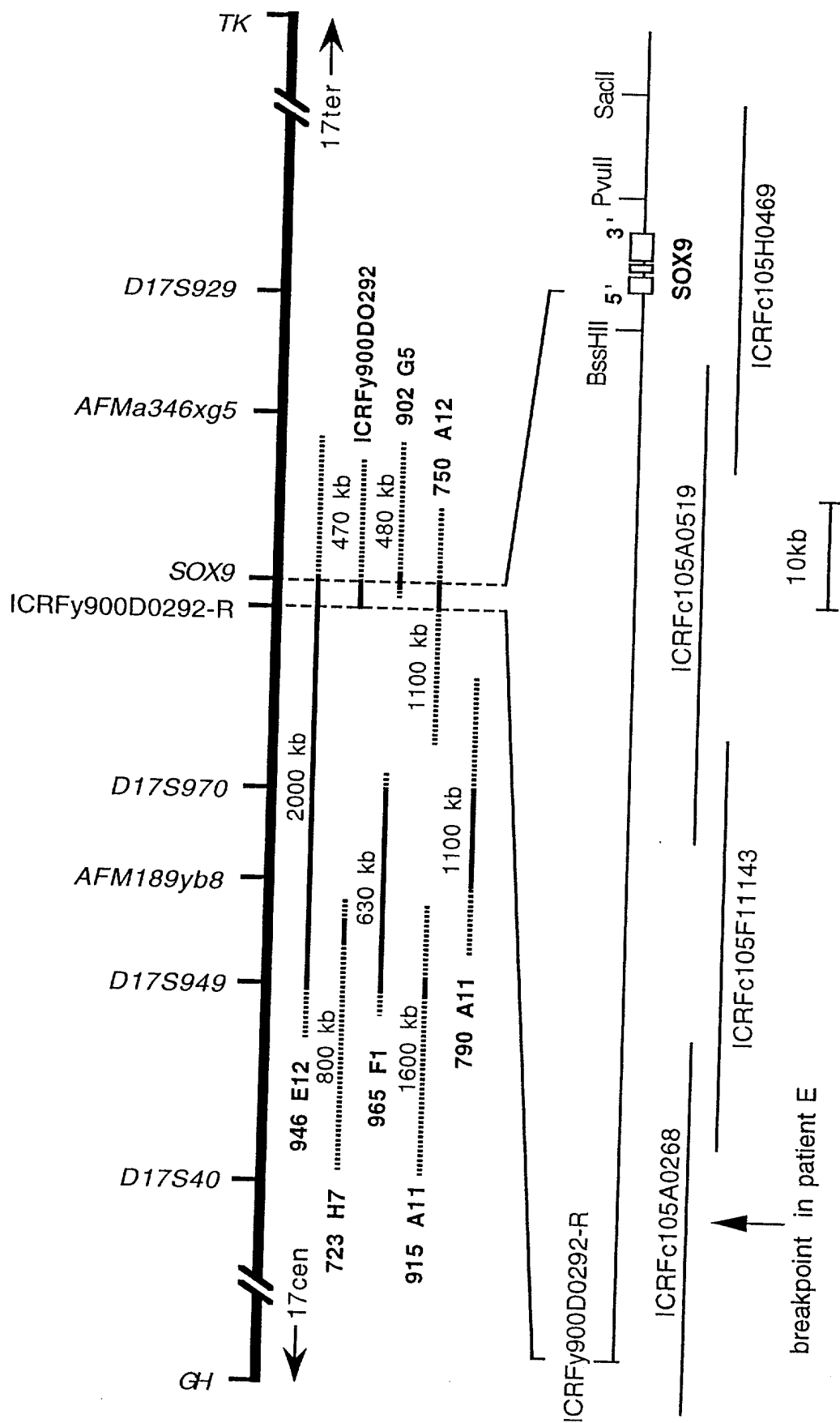


FIG. 7

CGGAGCTCGA	AACTGACTGG	AAACTTCAGT	GGCGCGGAGA	CTCGCCAGTT	TCAACCCCGG
AAACTTTTCT	TTGCAGGAGG	AGAAGAGAAG	GGGTGCAAGC	GCCCCCACTT	TTGCTCTTTT
TCCCTCCCCT	CTCCTCCTCT	CCAATTCCGC	TCCCCCACT	TGGAGCGGGC	AGCTGTGAAC
TGGCCACCCC	GCGCCTTCCT	AAGTGCTCGC	CGCGGTAGCC	GGCCGACGCG	CCAGCTTCCC
CGGGAGCCGC	TTGCTCCGCA	TCCGGGCAGC	CGAGGGGAGA	GGAGCCCGCG	CCTCGAGTCC
CCGAGCCGCC	GCGGCTTCTC	GCCTTTCCCC	GCCACCAGCC	CCCTGCCCCG	GGCCCCGCGT
TGAATCTCCT	GGACCCCTTC	ATGAAGATGA	CCGACGAGCA	GGAGAAGGGC	CTGTCCGGCG
CCCCCAGCCC	CACCATGTCC	GAGGACTCCG	CGGGCTCGCC	CTGCCCCGTC	GGCTCCGGCT
CGGACACCGA	GAACACGCGG	CCCCAGGAGA	ACACGTTCCT	CAAGGGCGAG	CCCCGATCTG
AGAAGGAGAG	CGAGGAGGAC	AAGTTCCCCG	TGTGCATCCG	CGAGGCGGTC	AGCCAGGTGC
TCAAAGGCTA	CGACTGGACG	CTGGTGCCCA	TGCCGGTGCG	CGTCAACGGC	TCCAGCAAGA
ACAAGCCGCA	CGTCAAGCGG	CCCATGAACG	CCTTCATGGT	GTGGGCGCAG	GCGGCGCGCA
GGAAGCTCGC	GGACCAGTAC	CCGCACCTGC	ACAACGCCGA	GCTCAGCAAG	ACGCTGGGCA
AGCTCTGGAG	ACTTCTGAAC	GAGAGCGAGA	AGCGGCCCTT	CGTGGAGGAG	GCGGAGCGGC
TGCGCGTGCA	GCACAAGAAG	GACCACCCGG	ATTACAAGTA	CCAGCCGCGG	CGGAGGAAGT
CGGTGAAGAA	CGGGCAGGCG	GAGGCAGAGG	AGGCCACGGA	GCAGACGCAC	ATCTCCCCCA
ACGCCATCTT	CAAGGCGCTG	CAGGCCGACT	CGCCACACTC	CTCCTCCGGC	ATGAGCGAGG
TGCACTCCCC	CGGCGAGCAC	TCGGGGCAAT	CCCAGGGCCC	ACCGACCCCA	CCCACCACCC
CCAAAACCGA	CGTGCAGCCG	GGCAAGGCTG	ACCTGAAGCG	AGAGGGGCGC	CCCTTGCCAG
AGGGGGGCG	ACAGCCCCCT	ATCGACTTCC	GCGACGTGGA	CATCGGCGAG	CTGAGCAGCG
ACGTCTATCT	CAACATCGAG	ACCTTCGATG	TCAACGAGTT	TGACCAGTAC	CTGCCGCCCA
ACGGCCACCC	GGGGGTGCCG	GCCACGCACG	GCCAGGTCAC	CTACACGGGC	AGCTACGGCA
TCAGCAGCAC	CGCGGCCACC	CCGGCGACCG	CGGGCCACGT	GTGGATGTCC	AAGCAGGAGG
CGCCGCGGCC	ACCCCCGCG	CAGCCCCCAC	AGGCCCCGCG	GGCCCCGCG	GCGCCCCCGC
AGCCGCAGGC	GGCGCCCCCA	CAGCAGCCGG	CGGCACCCCC	GCAGCAGCCA	CAGGCGCACA
CGCTGACCAC	GCTGAGCAGC	GAGCCGGGCC	AGTCCCAGCG	AACGCACATC	AAGACGGAGC
AGCTGAGCCC	CAGCCACTAC	AGCGAGCAGC	AGCAGCACTC	GCCCCAACAG	ATCGCCTACA
GCCCCCTCAA	CCTCCCACAC	TACAGCCCCT	CCTACCCGCC	CATCACCCGC	TCACAGTACG
ACTACACCGA	CCACCAGAAC	TCCAGCTCCT	ACTACAGCCA	CGCGGCAGGC	CAGGGCACC
GCCTCTACTC	CACCTTCACC	TACATGAACC	CCGCTCAGCG	CCCCATGTAC	ACCCCCATCG
CCGACACCTC	TGGGGTCCCT	TCCATCCCGC	AGACCCACAG	CCCCCAGCAC	TGGGAACAAC
CCGTCTACAC	ACAGCTCACT	CGACCTTGAG	GAGGCCTCCC	ACGAAGGGCG	ACGATGGCCG
AGATGATCCT	AAAAATAACC	GAAGAAAGAG	AGGACCAACC	AGAATTCCCT	TTGGACATTT
GTGTTTTTTT	GTTTTTTTAT	TTTGTTTTGT	TTTTTCTTCT	TCTTCTTCTT	CCTTAAAGAC
ATTTAAGCTA	AAGGCAATC	GTACCCAAAT	TTCCAAGACA	CAAACATGAC	CTATCCAAGC
GCATTACCCA	CTTGTTGGCC	ATCAGTGGCC	AGGCCAACCT	TGGCTAAATG	GAGCAGCGAA
ATCAACGAGA	AACTGGACTT	TTTAAACCCT	CTTCAGAGCA	AGCGTGAGG	ATGATGGAGA
ATCGTGTGAT	CAGTGTGCTA	AATCTCTCTG	CCTGTTTGGA	CTTTGTAATT	ATTTTTTTAG
CAGTAATTAA	AGAAAAAGT	CCTCTGTGAG	GAATATTCTC	TATTTTAAAT	ATTTTFTAGTA
TGTACTGTGT	ATGATTCAAT	ACCATTTTGA	GGGGATTTAT	ACATATTTTT	AGATAAAATT
AAATGCTCTT	ATTTTTCCAA	CAGCTAAACT	ACTCTTAGTT	GAACAGTGTG	CCCTAGCTTT
TCTTGCAACC	AGAGTATTTT	TGTACAGATT	TGCTTTCTCT	TACAAAAAGA	AAAAAAAAT
CCTGTTGTAT	TAACATTTAA	AAACAGAATT	GTGTTATGTG	ATCAGTTTTG	GGGGTTAACT
TTGCTTAATT	CCTCAGGCTT	TGCGATTTAA	GGAGGAGCTG	CCTTAAAAAA	AAATAAAGGC
CTTATTTTGC	AATTATGGGA	GTAAACAATA	GTCTAGAGAA	GCATTTGGTA	AGCTTTATGA
TATATATATT	TTTTTAAAGAA	GAGAAAAACA	CCTTGAGCCT	TAAAACGGTG	CTGCTGGGAA
ACATTTGCAC	TCTTTTAGTG	CATTTCTCTC	TGCCTTTGCT	TGTTCACTGC	AGCTTTAAGA
AAGAGGTAAA	AGGCAAGCAA	AGGAGATGAA	ATCTGTTCTG	GGAATGTTTC	AGCAGCCAAT
AAGTGCCCGA	GCACACTGCC	CCCGGTTGCC	TGCCTGGGCC	CCATGTGGAA	GGCAGATGCC
TGCTCGCTCT	GTCACCTGTG	CCTCTCAGAA	CACCAGCAGT	TAACCTTCAA	GACATTCAC

Figure 8a(1)

TTGCTAAAAT	TATTTATTTT	GTAAGGAGAG	GTTTTAATTA	AAACAAAAAA	AAATTCTTTT
TTTTTTTTTT	TTTTCCAATT	TTACCTTCTT	TAAAATAGGT	TGTTGGAGCT	TTCTCCTCAAAG
GGTATGGTCA	TCTGTTGTTA	AATTATGTTC	TTAACTGTAA	CCAGTTTTTT	TTTATTTTATC
TCTTTAATCT	TTTTTTATTAT	TAAAAGCAAG	TTTCTTTGTA	TTCTCACC	TAGATTTGTA
TAAATGCCTT	TTTGTCCATC	CCTTTTTTCT	TTGTTGTTTT	TGTTGAAAAC	AACTGGAAA
CTTGTTTCTT	TTTTTGATATA	AATGAGAGAT	TGCAAATGTA	GTGTATCACT	GAGTCATTTG
CAGTGTTTTT	TGCCACAGAC	CCTTGGGCTG	CCTTATATTG	TGTGTGTGTG	TGGGTGTGTG
TGTGTTTTGA	CACAAAAACA	ATGCAAGCAT	GTGTCATCCA	TATTTCTCTA	CATCTTCTCT
TGGAGTGAGG	GAGGCTACCT	GGAGGGGATC	AGCCCACTGA	CAGACCTTAA	TCTTAATTAC
TGCTGTGGCT	AGAGAGTTTG	AGGATTGCTT	TTTAAAAAAG	ACAGCAAAC	TTTTTTTTTTA
TTTAAAAAAA	GATATATTAA	CAGTTTTFAGA	AGTCAGTAGA	ATAAAATCTT	AAAGCACTCA
TAATATGGCA	TCCTTCAATT	TCTGTATAAA	AGCAGATCTT	TTTAAAAAAG	ATACTTCTGT
AACTTAAGAA	ACCTGGCATT	TAAATCATAT	TTTGTCTTTA	GGTAAAAGCT	TTGGTTTGTG
TTCGTGTTTT	GTTTGTTTCA	CTTGTTTCCC	TCCCAGCCCC	AAACCTTTTG	TTCTCTCCGT
GAAACTTACC	TTTCCCTTTT	TCTTCTCTT	TTTTTTTTTTG	TATATTATTG	TTTACAATAA
ATATACATTG	CATTAAAAAG	AAA			

Figure 8a(2)

Leu	Ser	Ser	Glu	Pro	Gly	Gln	Ser	Gln	Arg	Thr	His	Ile	Lys	Thr	Glu
385					390					395					400
Gln	Leu	Ser	Pro	Ser	His	Tyr	Ser	Glu	Gln	Gln	Gln	His	Ser	Pro	Gln
				405					410						415
Gln	Ile	Ala	Tyr	Ser	Pro	Phe	Asn	Leu	Pro	His	Tyr	Ser	Pro	Ser	Tyr
			420					425						430	
Pro	Pro	Ile	Thr	Arg	Ser	Gln	Tyr	Asp	Tyr	Thr	Asp	His	Gln	Asn	Ser
		435					440					445			
Ser	Ser	Tyr	Tyr	Ser	His	Ala	Ala	Gly	Gln	Gly	Thr	Gly	Leu	Tyr	Ser
	450					455					460				
Thr	Phe	Thr	Tyr	Met	Asn	Pro	Ala	Gln	Arg	Pro	Met	Tyr	Thr	Pro	Ile
465					470					475					480
Ala	Asp	Thr	Ser	Gly	Val	Pro	Ser	Ile	Pro	Gln	Thr	His	Ser	Pro	Gln
				485					490						495
His	Trp	Glu	Gln	Pro	Val	Tyr	Thr	Gln	Leu	Thr	Arg	Pro			
			500					505							

Figure 8a(4)

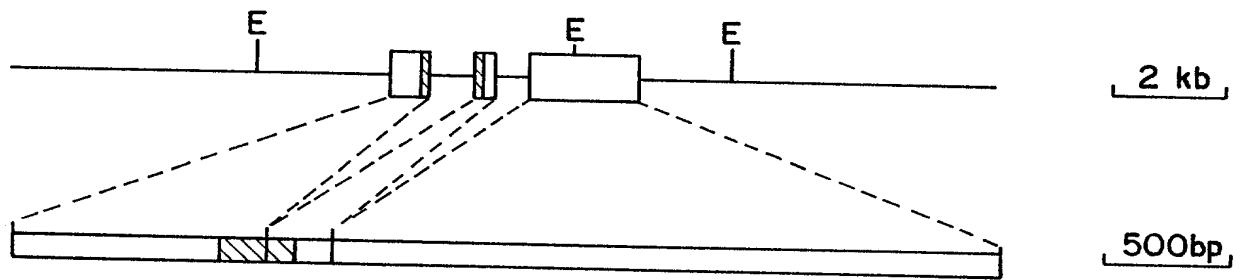


FIG.8b

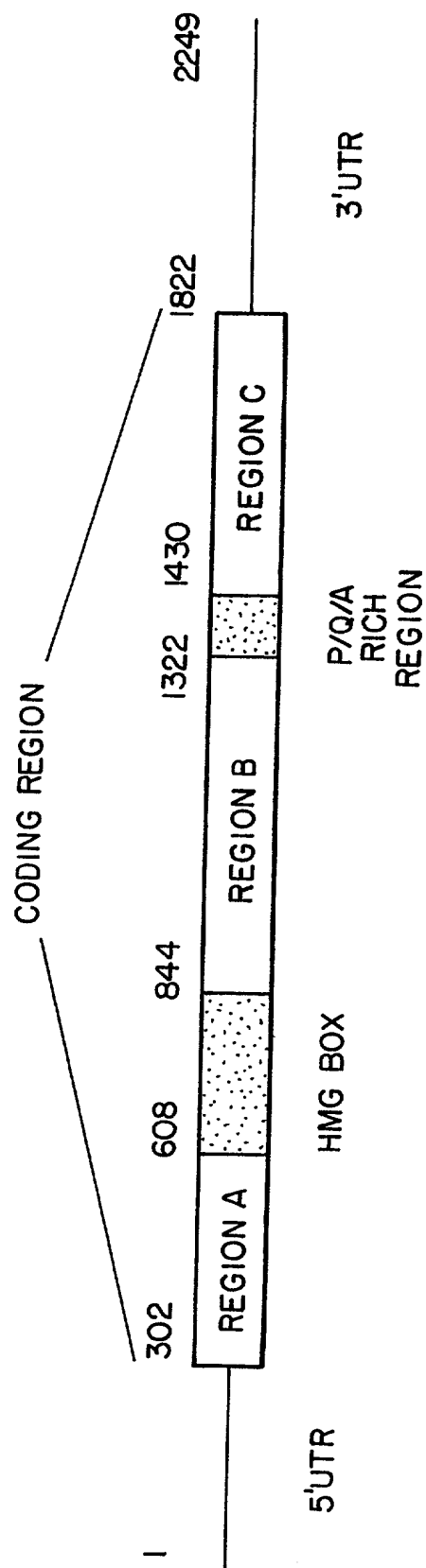


FIG.9

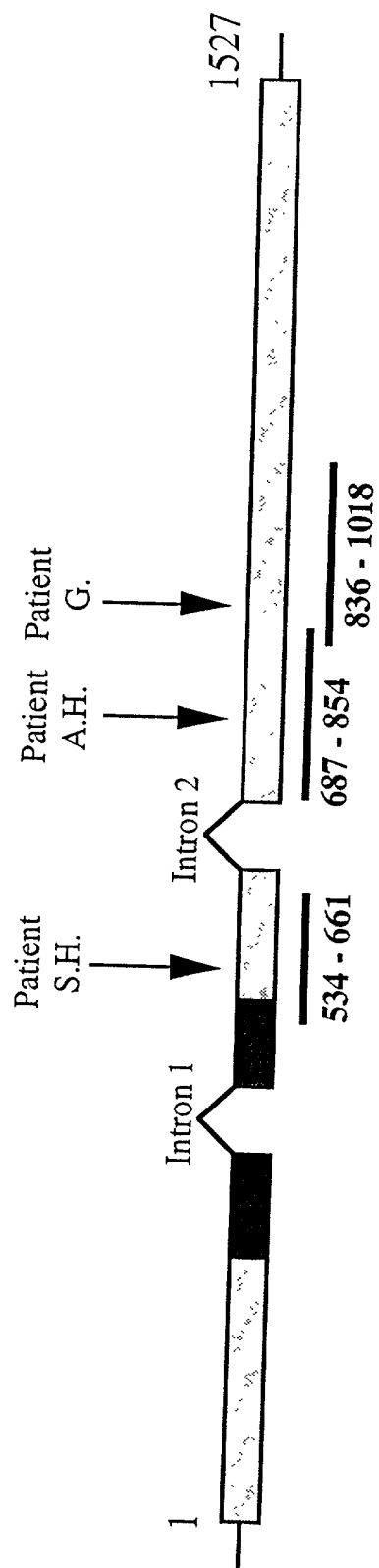
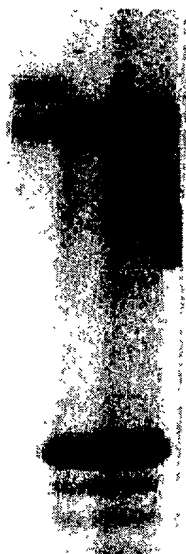


FIG. 10a

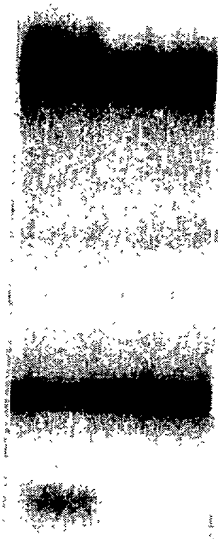
Patient S.H.

1 2 3



Patien A.H.

1 2 3



Patient G.

1 2 3

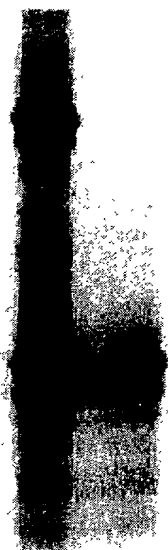


FIG.10b

